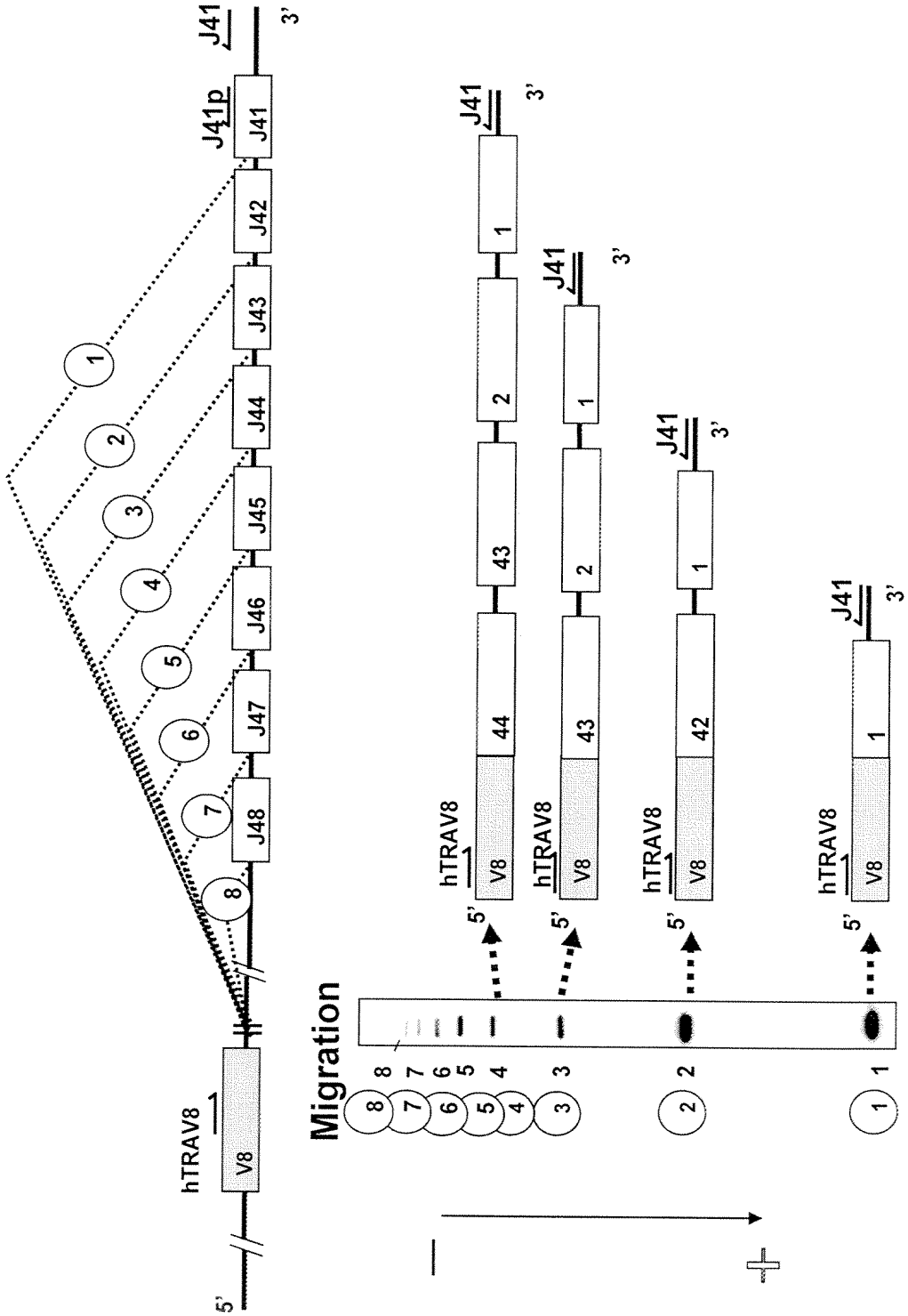


Figure 4



hV gene	Heptamer	SEQ ID NO	%	Spacer	SEQ ID NO	%	Nonamer	SEQ ID NO	%	RSS score	Dist/Cα (Kb)	Signal Qty	J tropism
hV1-1	CACAGTG	76	100	ACTATGAGGCGCTCTTAACTGTG	77	56	CCAAAATTG	78	56	72	925	1604	J10
hV1-2	CACGGTG	79	86	ACTATGAGGCGCTCTTAACTGCA	80	63	CCAAAATTG	78	56	69	904		J10
hV2	CACAGAG	81	86	GCAGGGAACCCCATGAACAGCTGA	82	56	ACAGAAACA	83	78	75	835	1637	J10
hV3	CACACTG	84	86	ATAGGGGCTGCAGCGGCGAGAGA	85	56	ACACAAACT	86	89	80	824	1940	J10
hV5	CACATTG	87	86	CTTCTCAGGCACTGTATCCTGT	88	94	ACCCAAACC	89	100	93	798	2406	J10
hV8-2	CACAGTG	76	100	CTTGAGACTGCAGGACAGCTGAA	90	50	CACAAGCCT	91	33	63	701		All J area
hV8-4	CACAGTG	76	100	CTTGAGACTGCAGGACAGCTGAA	90	50	CATAAACCT	92	33	63	653	15830	
hV8-6	CACAGTG	76	100	CCTGAGACTGCAGGACAGCTGAA	93	44	CACAACCT	94	44	65	569		
hV26-2	CACAGTG	76	100	GGACAGATGGGGCTGCAGCTGTG	95	56	CAATATCTC	96	33	64	345	5638	J48
hV35	CACAGTG	76	100	CTCCCAGAACACCTGCAGCCTGT	97	94	ACTCAAACCT	98	78	90	326	6520	J48
hV38-2	CACAGTG	76	100	AGACAAGCAACAGGACAGGCTT	99	31	ACAGAAACC	100	89	78	267	11008	J48
hV40	CACITGTG	101	86	TAAAAAGCACAGTGGAGGTATA	102	44	CAAAAACCT	103	44	60	233	6930	J48
hV41	CACAGTG	76	100	CTCCCAGGCACTGGAGGCCGT	104	94	ACCTAAACT	105	78	90	227	5630	J48
Consensus	CACAGTG	76		-T - - CAG-CA-CTG-AACTGT G GC GG	106		ACACAAACC C	89		%			

FIGURE 5